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(A) Hi-C data generation

Hi-C data is generated using a Hi-C kit. The process involves cross-linking chromatin, digesting it with a restriction enzyme, ligating the fragments, and sequencing the resulting DNA. The output is a Hi-C matrix, which is a square matrix where each element represents the frequency of interactions between two genomic regions.

(B) Hi-C data analysis

The Hi-C matrix is analyzed to identify topologically associating domains (TADs) and loops. This is done by calculating the enrichment of interactions within a genomic region. The enrichment is calculated as the ratio of the observed frequency of interactions to the expected frequency of interactions. The expected frequency is calculated based on the marginal frequencies of the matrix.

(C) Hi-C data visualization

The Hi-C matrix and TADs are visualized using heatmaps and TAD plots. Heatmaps show the frequency of interactions between genomic regions. TAD plots show the enrichment of interactions within a genomic region. The enrichment is color-coded, with red indicating high enrichment and blue indicating low enrichment.

(D) Hi-C data interpretation

The Hi-C data is interpreted in the context of gene expression and chromatin architecture. TADs are associated with gene expression, with high enrichment indicating high expression. Chromatin architecture is also associated with gene expression, with high enrichment indicating high expression.

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